Spatial distribution of needle bright disease of *Pinus sylvestris* var. *mongolica*

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Abstract The spatial distribution pattern of needle bright disease was mathematically studied. The results showed that it is tally with negative binomial distribution. The infected area and damaged amount can be forecasted with this spatial distribution pattern. Through the study on probability distribution of spatial points for single tree, the method and equations for calculation of the disease index of whole forest belt were determined.

Key words: *Pinus sylvestris* var. *mongolica*, Disease, *Septoria pini-putnilae* Sawada, *Dothistroma pipi* Hulbary, Needle bright, Spatial distribution

Materials and methods

Probability distribution pattern

Investigation methods

The space distribution of needle bright was investigated in Honghuarerji Forest Farm and Huihe Forest Farm from June to July in 1996. The elevation of the study areas is 700-1100 m. The age of the trees are 24~35 a. Canopy densities ranged from 0.4 to 0.7. There were no shrubs on forest floor. Totally 12 plots were set up and 30 trees for each plot were investigated. The information was reported according to Table1.

Poisson distribution:

$$Np_r = Ne^{-m} \times \frac{m^r}{r!} \tag{1}$$

$$\sum Np_r = Ne^{-m} (1 + m + \frac{m^2}{2!} + \frac{m^3}{3!} + \dots + \frac{m^r}{r!})$$
 (2)

Where: m is total average value, which can be calculated by $x = \sum fx/N$; Np_r is theoretical frequency.

The theoretical value was worked out one by one according to formula 1, then X^2 -test with the freedom degree n-2 was carried out.

Negative binomial distribution:

The theoretical expression pattern of negative binomial distribution is

$$Np_r = N_{(q-p)}^{-k} \tag{3}$$

Expanding the formula (3), then,

$$Np_{r} = N \frac{(k+r-1)!}{r!(k-1)!} q^{-k-r} p^{r}$$
(4)

Where: k, p and q are parameters that can be found out by the moment method and likelihood estimation. Moment method

$$k = \frac{\overline{x}}{D} \tag{5}$$

$$p = \frac{s^2}{\overline{r} - 1} \tag{6}$$

$$q = 1 + p \tag{7}$$

Where: s^2 – variance; \bar{x} --sample average value

Maximum likelihood estimation

$$Z_{i} = \sum_{x=0}^{r} \frac{A_{x}}{k_{i} + x} - A \ln(1 + \frac{\overline{x}}{k_{i}})$$
 (8)

Where: $Z_i = 0$, k is being selected, and

$$Ax = \sum_{i=1}^{r} f_i \tag{9}$$

Where: Ax is the sum of accumulated investigations for >x, f_i is a frequency of i appears in samples; r is the maximum group number.

$$\hat{k} = \hat{k}_2 + \frac{\hat{k}_1 - \hat{k}_2}{h_1 - h_2} (h_1 - h_2)$$
 (10)

$$p = \frac{\overline{x}}{k} \tag{11}$$

$$q = 1 + p \tag{12}$$

Iwao (1968, 1977) m m regression

$$m = \alpha \times \beta \, \overline{m} \tag{13}$$

$$\dot{m} = \overline{m} + \left(\frac{s^2}{\overline{m}} - 1\right) \tag{14}$$

Where: α is average crowding level of distributed basic elements by size. If α =0, the basic element of the distribution is individual. If α > 0, individuals attract each other and the basic element is individual group. If α < 0, the individuals repel each other. β represents the spatial distribution pattern of basic element. When β =1, it is random distribution, β >1, even distribution, β <1, aggregation distribution. When α =0, β =1, the basic element is individual and accords with random distribution. When α >1, β =1, individual group is random distribution and the size of individual group is fixed. When α =0, β >1, it is true of negative binomial distribution with a common K value. When α =0, β <1, it is even distribution. If α >0, β >1, there is no model.

Improved Iwao \dot{m} -m model

$$m = \alpha' + \beta' \overline{m} + \gamma' \overline{m}^2 \tag{15}$$

Where: α' is an average crowding level of the individuals in the basic elements; β' is relative aggregation degree of the basic elements under low density; γ is the rate of the relative aggregation of the basic elements which changes with population density.

Nevman distribution

$$Np_0 = Ne^{-m_1 c m_1 f_{(6)}} (16)$$

$$Np_{r+1} = N \frac{m_1}{r+1} \sum_{k=0}^{r} F_k p_{r-k}$$
 (17)

Where:

$$F_k = \frac{1}{k!} f_{(0)}^{(k+1)} \tag{18}$$

Where:

$$f_{(0)} = n!(-m_2)^{-n} \left\{ e^{-m_2} - \sum_{s=0}^{n-1} \frac{(-m_2)^2}{s!} \right\}$$
 (19)

$$f_{(0)} = (m_2 + n)f_{(0)} - n \tag{20}$$

If k > 1,

$$f_{(0)}^{k+1} = (m_2 + n + k) f_{(0)}^{(k)} - k m_2 f_{(0)}^{(k-1)}$$
 (21)

Then,

$$F_{0} = f_{(0)} = (m_{2} + n)f_{(0)} - n$$

$$F = \{(m_{2} + n)^{2} + n\}f_{(0)} - n\{(m_{2} + n) + 1\}$$
(22)

If k<1,

$$F_k = \frac{m_2 + n + k}{k} F_{k-1} - \frac{m_2}{k - 1} F_{k-2}$$
 (23)

Where:

$$m_2 = \frac{(n+2)(s^2 - \bar{x})}{2\bar{x}} \tag{24}$$

$$m_1 = \frac{(n+1)\overline{x}}{m_2} \tag{25}$$

Probability distribution of spatial points for single tree

Investigation Methods

One sample plot was chosen in the plantation (25 year-old, canopy density 0.6) at Honghuaerji Forest Farm and the other plot was chosen in seed-bearer forest (35 year-old, canopy density 0.4) at Huihe Forest Farm. Eight sample trees were selected randomly in the plots. The sample trees were defined as the top, middle and bottom layers according to north, south, east and west sides respectively. So 12 sample branches were chosen. The top, middle and bottom layers were also determined for each branch. A small branch of 20 cm in length on each layer was chosen to pick up leaves and check the disease. The data was counted according to "rating standard of disease index" (Table 1).

Table 1. Rating standard of disease index

Disease Defined rating value		Infected degree					
I	0	No disease spots on leaf					
II	1	Less than 1/5 leaf area infected					
Ш	2	1/5∼1/3 leaf area infected					
IV	3	1/3∼2/3 leaf area infected					
V	4	More than 2/3 leaf area infected					

Research Methods

We took the ground surface as a horizontal, the

northern side as Y axis and eastern side as X axis. We made tangent lines of a tree from farthest point of the low layer branch of north to that of east. From the intersection of tow lines to the ground was defined as Z axis(upturned). Thus a spatial right angle coordinate was established. The probability of pine needle bright (f) was calculated out for each point at the spatial right angle coordinate, then, the coordinate of every point is corresponding to the probability f.

We take the X, Y and Z as independent variables and F as variable to set up the regression model:

$$F = A + BX + CY + DZ \tag{26}$$

$$F = nA + B \sum X + C \sum Y + D \sum Z$$

$$X \sum F = A \sum X + B \sum X^{2} + C \sum XY + D \sum XZ$$

$$Y \sum F = A \sum Y + B \sum XY + C \sum Y^{2} + D \sum YZ$$

$$Z \sum F = A \sum Z + B \sum XZ + C \sum YZ + D \sum Z^{2}$$

$$(27)$$

Results and analysis

Spatial distribution pattern of probability Poisson Distribution

Infected leaves (x)	Frequency of investigation(f)					(fx)		(fxx)			
	1	2	3	4	1	2	3	4	1	2	3	4
0	57	50	57	84	0	0	0	0	0	0	0	0
1	14	16	68	120	14	16	68	120	14	16	68	120
2	25	28	54	109	50	56	108	218	100	112	216	436
3	17	21	61	69	51	63	183	207	153	189	549	621
4	12	32	44	36	48	128	176	144	192	512	704	576
5	17	20	41	36	85	100	205	180	425	500	1025	900
6	22	33	40	31	132	198	240	186	792	1188	1440	1116
7	21	32	33	25	147	224	232	175	1029	1568	1617	122
8	18	34	26	19	144	272	208	152	1152	2176	1664	121
9	16	15	25	17	144	135	225	153	1296	1215	2025	137
10	22	9	14	9	220	90	140	90	2200	900	1400	900
11	18	13	15	5	198	143	165	55	2178	1573	1815	605
12	20	25	10	4	240	300	120	48	2880	3600	1440	576
13	14	8	9	3	182	104	117	39	2366	1352	1521	507
14	18	19	13	1	252	266	182	14	3528	3724	2548	196
15	11	12	9	1	165	180	135	15	2475	2700	2025	225
16	13	18	9	1	208	288	144	16	3328	4608	2304	225
17	9	15	12	0	153	255	204	0	2601	4335	3468	0
18	14	12	10	0	252	216	180	0	4536	3888	3240	0
19	12	18	6	1	228	342	114	19	4332	6498	2166	361
20	7	7	1	2	140	140	20	40	2800	2800	400	800
21	13	22	1	1	273	462	21	21	5733	9702	441	44
22	5	7	2	0	110	154	44	0	2420	3388	968	0
23	13	8	1	0	299	184	23	0	6877	4232	529	0
24	10	4	1	0	240	96	24	0	5760	2304	576	0
25	6	3	2	0	150	75	50	0	3750	1875	1250	0
26	8	5	2	0	208	130	52	0	5408	3380	1352	0
27	10	12	2	0	270	324	54	0	7290	8748	1458	0
28	12	9	0	0	336	252	0	0	9408	7056	0	0
29	8	5	2	0	232	145	58	0	6728	4205	1682	0
30	1	2	0	0	30	60	0	0	900	1800	0	0
31	8	11	0	0	248	341	0	0	7688	10571	.0	0
32	7	7	0	0	224	224	0	0	7168	7168	0	0
33	3	2	1	0	99	66	33	0	3267	2178	1089	0
34	4	3	0	0	136	102	0	0	4624	3468	0	0
35	4	1	0	0	140	35	0	0	4900	1225	0	0
36	4	3	0	0	144	108	0	0	5184	3888	0	0
37	4	6	1	0	148	222	37	0	5476	8214	1369	0
38	3	3	0	0	114	114	0	0	4332	4332	0	0

Continued Table 2

Infected	Fre	quency of	investigat		(f)	<)		(fxx)				
leaves (x)	1	2	3	4	1	2	3	4	1	2	3	4
39	2	3	0	0	78	117	0	0	3042	4563	0	0
40	2	0	0	0	80	0	0	0	3200	0	0	0
41	1	0	0	1	41	0	0	41	1681	0	0	1681
42	3	1	0	0	126	42	0	0	5292	1764	0	0
43	2	2	0	0	86	86	0	0	3698	3698	0	0
44	2	0	0	0	88	0	0	0	3872	0	0	0
46	1	0	0	0	46	0	0	0	2116	0	0	0
47	2	0	0	0	94	0	0	0	4418	0	0	0
48	1	1	0	0	48	48	0	0	2304	2304	0	0
49	2	2	1	0	98	98	49	0	4802	4802	2401	0
50	0	1	0	0	0	50	0	0	0	2500	0	0
51	3	0	0	0	153	0	0	0	7803	0	0	0
52	1	2	0	0	52	104	0	0	2704	5408	2166	0
53	1	1	0	0	53	53	0	0	2809	2809	400	0
54	3	0	0	0	162	0	0	0	8748	0	441	0
56	3	0	0	0	168	0	4	0	9408	0	968	0
59	2	0	0	0	118	0	0	0	6962	0	529	0
61	2	0	0	0	122	0	0	0	7442	0	576	0
62	2	0	0	0	124	0	0	0	7688	0	1250	0
63	1	0	0	0	63	0	0	0	3969	0	1352	0
64	1	0	0	0	64	0	0	0	4096	0	1458	0
65	1	0	0	0	65	0	0	0	4225	0	0	0
67	0	1	0	0	0	67	0	0	0	4489	1682	0
71	1	0	0	0	71	0	0	0	5041	0	0	0
72	4	0	0	0	288	0	0	0	20736	0	0	0
73	2	0	0	0	146	0	0	0	10658	0	0	0
75	1	0	0	0	75	0	. 0	0	5625	0	0	0
76	• 1	0	0	0	76	0	0	0	5776	0	0	0
78	1	0	0	0	78	0	0	0	6048	0	0	0
81	1	0	0	0	81	0	0	0	6561	0	0	0
84	3	0	0	0	252	0	0	0	21168	0	0	0
85	2	0	0	0	170	0	0	0	14450	0	0	0
86	1	0	0	0	86	0	0	0	15842	0	0	0
89	2	0	0	0	178	0	0	0	8281	0	0	0
91	1	0	0	0	91	0	0	0	17677	0	0	0
94	2	0	0	0	188	0	0	0	9025	0	0	0
95	1	0	0	0	95	0	0	0	18432	0	C	0
96	2	٥	0	0	192	0	0	0	10816	0	0	0
104	1	0	0	0	104	0	0	٥	11025	0	0	0
105	1	0	0	0	104	0	0	0	0	0	0	0
109	0	1	0	0	0	0	0	0	14400	0	0	0
120	1	0	0	0	120	0	0	0	15625	0	0	0
125	1	0	0	0	125	0	0	0	16129	0	0	0
127	1	0	0	0	127	0	0	٥	19321	0	0	0
139	1	0	0	0	139	0	0	0	495632	0	0	0
Σ	569	565	580	575	11170	7384	3961	1933	2809	175406	62349	14135

From formula (1), (2) and (3) we can obtain the theoretical value, then make X^2 -text to this theoretical value with the formula as follows:

$$X^{2} = \sum \{ \frac{(f - f_{c})^{2}}{f_{c}} \}$$
 (28)

 $X^2 = 3.47$

With a confidence of 0.95 and a freedom degree of 83, the result of X^2 test is $X^2 \approx 9.3$ °, which does not

accord with Poisson distribution.

According with negative binomial distribution
According to Table 2 the calculation method is taken
as follows:

(i) Using moment method to estimate k value:

By formula (5), (6), (7), That is p = 0.25, q = 1.27, k = 84.2.

With a confidence 0.95 and freedom degree 83, the result of X^2 -test accords with negative binomial distribution.

(ii) Using maximum likelihood estimation to estimate k value

According to formula (10), (11), (12), that is p = 0.43, q = 1.43, k = 78.3.

With a confidence 0.95 and a freedom degree 83, the result of X^2 -test accords with negative binomial distribution.

Iwao m -m distribution

By formula (13), (14), $\alpha = 0$, $\beta = 1.35$.

By formula (15), $\alpha = 23.5$, $\beta = 1.73$, r = 53.5.

With a confidence 0.95 and a freedom degree 83, the result of X^2 -test does not accord with Iwao $\dot{m} - m$ distribution.

Neyman distribution

By formula (16) and (17), that is F' = 1583.35

With a confidence 0.95 and a freedom degree 83, the result of X^2 -test does not accord with Neyman distribution.

Probability distribution pattern of spatial points for single tree

Sixteen regression equations were set up, which represent the probability at a certain point (Table 3).

Table 3. The probability distribution of single tree space

Number of tree	Regression equation of each sample tree
01	F=0.0134X + 0.235Y + 0.0459Z- 1.374
02	F=0.0172X + 0.132Y + 0.0537Z - 1.452
03	F=0.0334X + 0.251Y + 0.0347Z - 1.278
04	F=0.0243X + 0.373Y + 0.0226Z - 1.384
05	F=0.0337X + 0.284Y + 0.0414Z - 1.252
06	F=0.0236X + 0.571Y + 0.0394Z - 1.234
07	F=0.0197X + 0.154Y + 0.0135Z - 1.285
08	F=0.0091X + 0.075Y + 0.0421Z 1.137
09	$F=0.0144X_1+0.134Y+0.0126Z-1.453$
10	F=0.0142X + 0.284Y + 0.0092Z - 1.462
11	F=0.0433X + 0.156Y + 0.0237Z - 1.243
12	F=0.0126X + 0.234Y + 0.0529Z - 1.172
13	F=0.0521X + 0.291Y + 0.0235Z - 1.423
14	F=0.0412X + 0.275Y + 0.0459Z - 1.361
15	F=0.0314X + 0.348Y + 0.0529Z - 1.524
16	F=0.0138X + 0.325Y + 0.0255Z - 1.341

The above 16 equations are for normal distribution.

The general regression equation is

$$F = 0.0248375X + 0.2625625Y + 0.03371875Z - 3359475$$

We find the sum for the probability of each sample point.

If
$$f_1=a+b\overline{x}$$
, $f_2=cy$, $f_3=dz$, and
$$F=f_1+f_2+f_3$$

Then, we find the indefinite integral of f_1 f_2 f_3 in X, Y, Z range respectively:

$$\int f_1 = \int \frac{a + bx = ax + bx^2 v}{2}$$

$$\int f_2 = \int cy = cy^2 / 2$$

$$\int f_3 = \int dz = dz^2 / 2$$

and set
$$F = \int f_1 + \int f_2 + \int f_3$$

F is the probability sum of every sample point of the whole tree, or the probability of infected leaves taking up the total leaf amount. The probability is regarded as theoretical disease index for single disease of the tree.

Conclusions

The needle bright disease was tally with negative binomial distribution. Using the sampling methods of this spatial distribution pattern, we can forecast if the disease occur and the infecting degree accurately.

Through the probability distribution pattern of spatial points for the single tree and finding the indefinite integral of the general regression equation, the disease index for the whole forest can be calculated out.

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